HUMAN TELOMERASE

```
ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAG     60
MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu     20

GTGCTGCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAG    120
ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln     40

CGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGG    180
ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp     60

GACGCACGGCCGCCCCCCGCCGCCCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTG    240
AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu     80

GTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGC    300
ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly    100

TTCGCGCTGCTGGACGGGGCCCGCGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGC    360
PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg    120

AGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTG    420
SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu    140

TTGCGCCGCGTGGGCGACGACGTGCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTG    480
LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal    160

CTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCT    540
LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla    180

GCCACTCAGGCCCGGCCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAA    600
AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu    200

CGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGT    660
ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly    220

GCGAGGAGGCGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGT    720
AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg    240
```

Fig. 1A

GGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGC 780
GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly 260

AGGACGCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAA 840
ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 280

GAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGC 900
GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300

CGCCAGCACCACGCGGGCCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCT 960
ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro 320

TGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAG 1020
CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln 340

CTGCGGCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTC 1080
LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360

GTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCC 1140
ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro 380

CGCCTGCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCAC 1200
ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis 400

GCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACC 1260
AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 420

CCAGCAGCCGGTGTCTGTGCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAG 1320
ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu 440

GAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAG 1380
GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln 460

GTGTACGGCTTCGTGCGGGCCTGCCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCC 1440
ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer 480

AGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCAT 1500
ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis 500

Fig. 1B

```
GCCAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGGCTGCGCTTGGCTG    1560
AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu     520

CGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATC    1620
ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle     540

CTGGCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTC    1680
LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe     560

TTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTC    1740
PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal     580

TGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAG    1800
TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu     600

CTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGA    1860
LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg     620

CTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTG    1920
LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal     640

GGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCA    1980
GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla     660

CTGTTCAGCGTGCTCAACTACGAGCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTG    2040
LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal     680

CTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAG    2100
LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln     700

GACCCGCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATC    2160
AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle     720

CCCCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGC    2220
ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys     740

GTGCGTCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAG    2280
ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys     760
```

Fig. 1C

AGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTG 2340
SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780

CAGGAGACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAG 2400
GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGlu 800

GCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATC 2460
AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle 820

AGGGGCAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTG 2520
ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840

CTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGAC 2580
LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp 860

GGGCTGCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCCACGCG 2640
GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880

AAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTG 2700
LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 900

CGGAAGACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTT 2760
ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 920

CAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTG 2820
GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu 940

GAGGTGCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTC 2880
GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960

AACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTG 2940
AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu 980

AAGTGTCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAAC 3000
LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000

ATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCA 3060
IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020

Fig. 1D

TTTCATCAGCAAGTTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCC 3120
PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAls 1040

TCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGC 3180
SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly 1060

GCCGCCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTC 3240
AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu 1080

AAGCTGACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAG 3300
LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100

ACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGCAGCCAAC 3360
ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAlaAsn 1120

CCGGCACTGCCCTCAGACTTCAAGACCATCCTGGACtgatggccacccgcccacagccag 3420
ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132

Gccgagagcagacaccagcagccctgtcacgccgggctctacgtcccagggagggagggg 3480
Cggcccacacccaggcccgcaccgctgggagtctgaggcctgagtgagtgtttggccgag 3540
gcctgcatgtccggctgaaggctgagtgtccggctgaggcctgagcgagtgtccagccaa 3600
gggctgagtgtccagcacacctgccgtcttcacttccccacaggctggcgctcggctcca 3660
ccccagggccagcttttcctcaccaggagcccggcttccactccccacataggaatagtc 3720
catccccagattcgccattgttcacccctcgccctgccctcctttgccttccacccccac 3780
catccaggtggagaccctgagaaggaccctgggagctctgggaatttggagtgaccaaag 3840
gtgtgccctgtacacaggcgaggaccctgcacctggatgggggtccctgtgggtcaaatt 3900
ggggggaggtgctgtgggagtaaaatactgaatatatgagtttttcagttttgaaaaaaa 3960
aaaa 3964

Fig. 1E

```
Euplotes    1 -----------------------MEVDVDNQADNHGIHSALKTCEEIKEAKTLYSWIQKVIRCR--NQSQSHYKDLEDIK
HT1         1 RRLGPQGWRLVQRGDPAAFRALVAQCLVCVPWDAR-PPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGA
EST2        1 ------------------------------------------------MKILFEFIQDKLDID--LQTNSTYKENLKCG

Euplotes   56 IFAQTNIVATPRDYNEEDFKVIARK---------EVFSTGLMIELIDKCLVELLSSSDVSDRQKLQCFGFQLKGNC-LAK
HT1        80 RGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAY---QVCGPPLYQLGAATQA
EST2       30 HFNGLDEILTT-CFALPNSRKIALP---------CLPGDLSHKAVIDHCIIYLLTGELYNN---VLTFGYKIARNEDVNN

Euplotes  126 THLLTALSTQKQYFFQDEWNQVRAMIGNELFRHLYTKYLIFQRTSEGTLVQFCGNNVFDHLKVNDKFDKKQKGGAADMNE
HT1       157 RPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRG
EST2       97 SLFCHSANVNVTLLKGAAWKMFHSLVGTYAFVDLLINYTVIQFNGQ-FFTQIVGNRCNEPHLPPKWVQRSSSS-------

Euplotes  206 PRCCSTCKYNVKNEKDHFLNNI------------------------------NVPNWNNMKSRTRIFYCTHFNRNNQFF
HT1       237 PSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDK--EQLR
EST2      169 ----SATAAQIKQLTEPVTN-----------------------------------------KQFLHKLNIN-SSSFF

Euplotes  255 KKHEFVSNKNNISAM-DRAQTIFTNI--------FRFNRIRKKLKDKVIEKIAYMLEKVKDFNFNYYLTKSCPLPENWRE
HT1       315 PSFLLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRY-WQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVTP
EST2      200 PYSKILPSSSSIKKLTDLREAIFP----------TNLVKIPQRLKVRINLTLQKLLKRHKRLNYVSILNSICPPLEGT--

                                                                     Telomerase domain
Euplotes  326 RK-----QKIENLINKTREEKS--KYYEELFSYTTDNKCVTQFINEFFYNILPKDFLTGR-NRKNFQKKVKKYVELNKHE
HT1       394 AAGVCAREKPQGSVAAPEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHA
EST2      268 ---------VLDLSHLSRQ---------------SPKERVLKFIIVILQKLLPQEMFGSKKNKGKIIKNLNLLLSLPLNG

Euplotes  398 LIHKNLLLEKINTREISWMQVET-SAKHFYYFDHENIYVLWKLLRWIFEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNIW
HT1       474 KLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVW
EST2      324 YLPFDSLLKKLRLKDFRWLFISD-IWFTKHNFENLN-QLAICFISWLFRQLIPKIIQTFFYCTEIS-STVTIVYFRHDTW

                                                   Motif 1  Motif2
Euplotes  477 DVIMKMSIADLKK-ETLAEVQEKEVEEWKKSL-GFAPGKLRLIPKKTT--FRPIMTFNKKIVNSDRK--TTKLTTNTKLL
HT1       554 SKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDG--LRPIVNMDYVVGARTFRREKRAERLTSRVK
EST2      401 NKLITPFIVEYFK-TYLVENNVCRNHNSYTLS-NFNHSKMRIIPKKSNNEFRIIAIPCRGADEEEFT--IYKENHKNAIQ
```

Fig. 2A

```
                                                                                      Motif A
Euplotes  551 NSHLMLKTLKN-RMFKDPFGFAVFNYDDVMKKYEEFVCKWKQVGQP-KLFFATMDIEKCYDSVNREKLSTFLKTTKLLSS
HT1       632 ALFSVLNYERARR--PGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQN
EST2      477 PTQKILEYLRNKRPTSFTKIYSPTQIADRIKEFKQRLLKKFNNVLP-ELYFMKFDVKSCYDSIPRMECMRILKDALKNEN

Euplotes  629 DFWIMTAQILKRKNNIVIDSKNFRKKEMKDYFRQKFQKIALEGGQYPTLFSVLENEQNDLNAKKTLIVEAK-CRNYFKKD
HT1       710 TYCVRRYAVVQKAAHGHVRKAFKSHVS-------------TLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSG
EST2      556 GFFVRSQYFFN-TNTGVLKLFNVVN---------------A--SRVPKPYELYIDNVRTVHLSNQDVINVV-EMEIFKT-

                               Motif B                                      Motif C
Euplotes  708 NLLQPVINICQYNYINFNGKFYKQTKGIPQGLCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLTDDYLLIT
HT1       777 LFDVFLRFMCHHAVRIR-GKSYVQCQGIPQGSILSTLLCSLCYGDMEN---KLFAGIRRD------GLLLRLVDDFLLVT
EST2      616 --ALWVEDKCYIR-----------EDGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPSQD------TLILKLADDFLIIS

                            Motif D                              Motif E
Euplotes  788 TQENNAVLFIEKLINVSRENGFKFNMKKLQTSFPLSPSKFAKYGMDSVEEQNIVQDYCDWIGISIDMKTLALMPNINLRI
HT1       847 PHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGG-TAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYAR--
EST2      677 TDQQ-QVINIKKLAMG----GFQKYNAKANRDKILAVS--------SQSDDDTVIQFCAMHIFVKELEVWKHSSTMN---

Euplotes  868 EGILCTLNLNMQTKKASMWLKKKLKSFLMNNITHYFRKTITTEDFANKTLNKLFISGGYKYMQCAKEY--KDHFKKNLAM
HT1       924 TSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLPFHQQVWKNPTF
EST2      741 -------NFHIRSKSS----KGIFRSLIALFNTRISYKTIDTNLNSTNTVLMQIDHVVKNISECYKSA--FKDLSINVTQ

Euplotes  946 SSMIDLEVSKIIYSVTRAFFKYLVCNIKDTIFGEEHYPDFFLSTLKHFIEIFSTKKYIFNRVCMILKAKEAKLKSDQCQS
HT1      1004 FLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLC-HQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGT
EST2      808 NMQFHSFLQRIIEMTVSG----CPITKCDPLIEYEVR--FTI--LNGFLESLSSNTSKF-KDNIILLRKEIQHLQAYIYI

Euplotes 1026 LIQYDA----------------
HT1      1083 TLTALEAAANPALPSDFKTILD
EST2      879 YIHIVN----------------
```

Fig. 2B

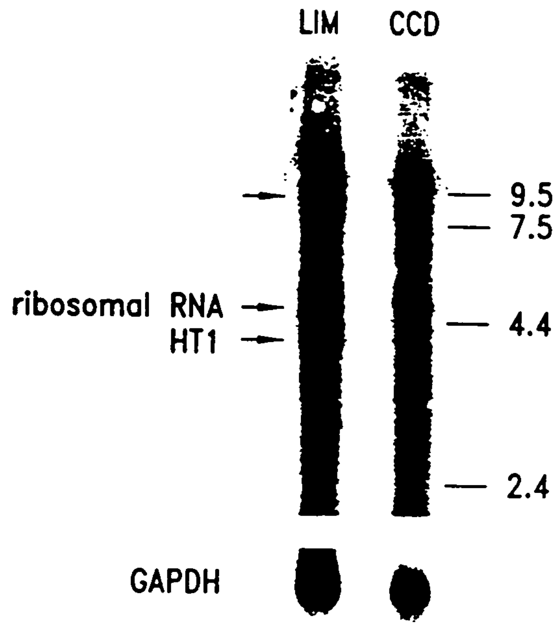

Fig. 3

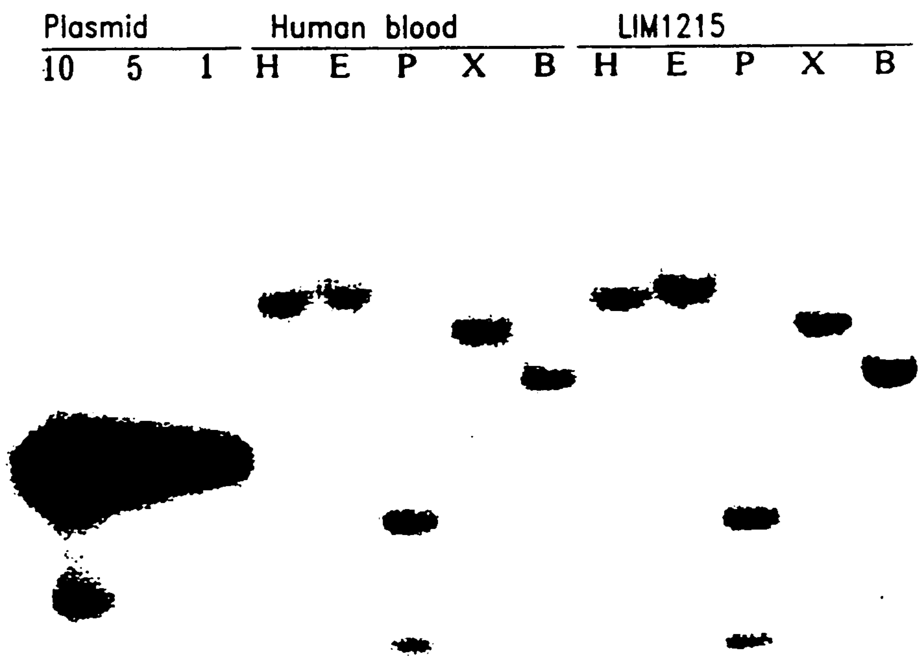

Fig. 4

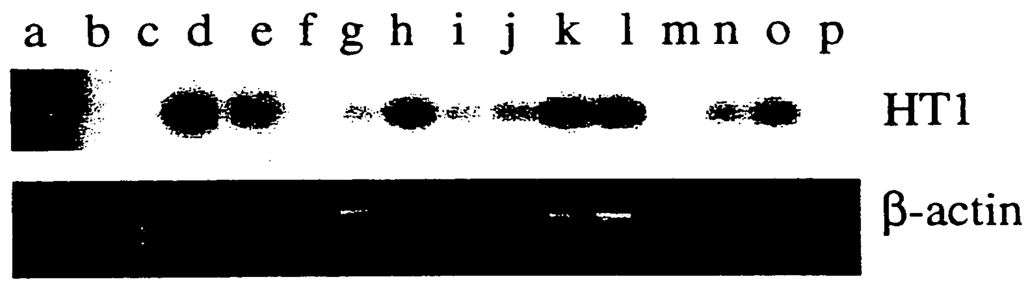

Fig. 5

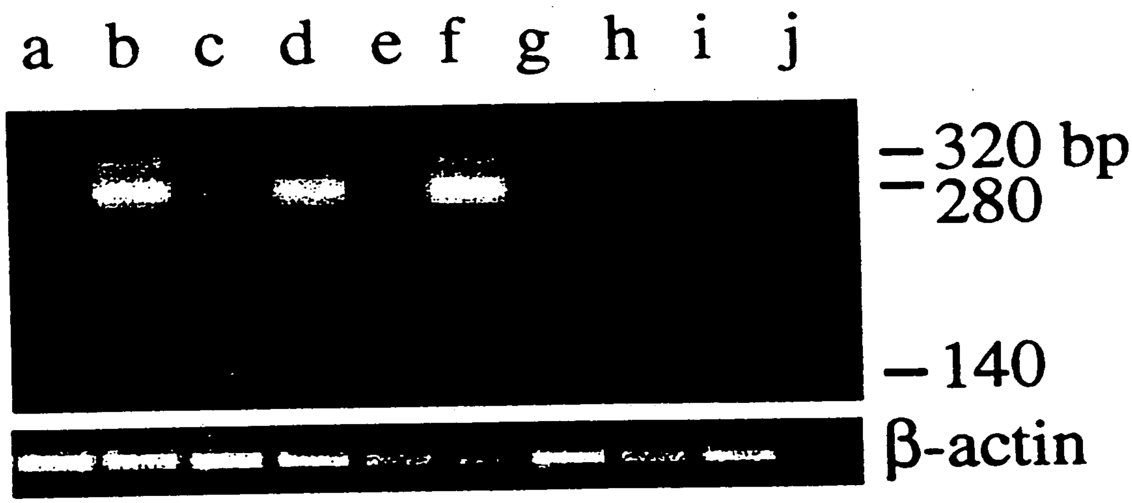

Fig. 6

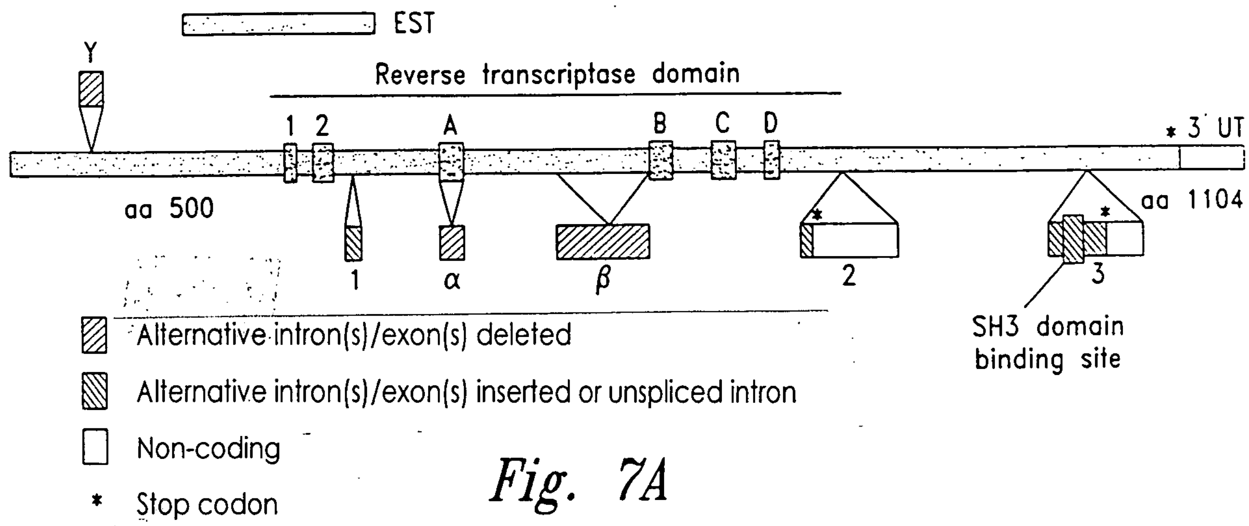

Fig. 7A

Variants:	1	α	β	2	3
RT–PCR product	NO	+	+	NO	+ & –
PCR from LIM1215 lib.	–	+	–	+	NO
RT–PCR product 53.2 cDNA	NO	–	+	NO	+
	–	–	–	–	NO

Fig. 7B

```
               222                                                          223
Y    5'-CCAGGTG|ggcctc                                         gcaggtg|TCCTGCC-3'

               1950                                                         1952
1    5'-AAAGAGG|GTGGCTG.................................AACAGAA|GCCGAGC-3'

               2130                                                         2167
a    5'-TGTCAAG|gtggatg.................................cccccag|GACAGGC-3'

               2286                                                         2468
b    5'-GAGCCAC|gtctcta.................................ggggcaa|GTCCTAC-3'

               2843                                                         2844
2    5'-ACTCCAG|GTGAGCG.................................XXXXXXX|CTATGCC-3'

               3157
3    5'-AACGCAG|CCGAAGAAAACATTTCTGTCGTGACTCCTGCGGTGCTTGGGTCGGGACAGCCAGAGATGG
          T  A  A   E  E  N  I  L  V  V  T  P  A  V  L  G  S  G  Q  P  E  M  E

                    AGCCACCCCGCAGACCGTCGGGTGTGGGCAGCTTTCCGGTGTCTCCTGGGAGGGGAGTTG
                      P  P  R  R  P  S  G  V  G  S  F  P  V  S  P  G  R  G  V  G

                                                              3158
                    GGCTGGGCCTGTGACTCCTCAGCCTCTGTTTTCCCCCAG|GGATGTC-3'
                      L  G  L  *
```

Fig. 7C

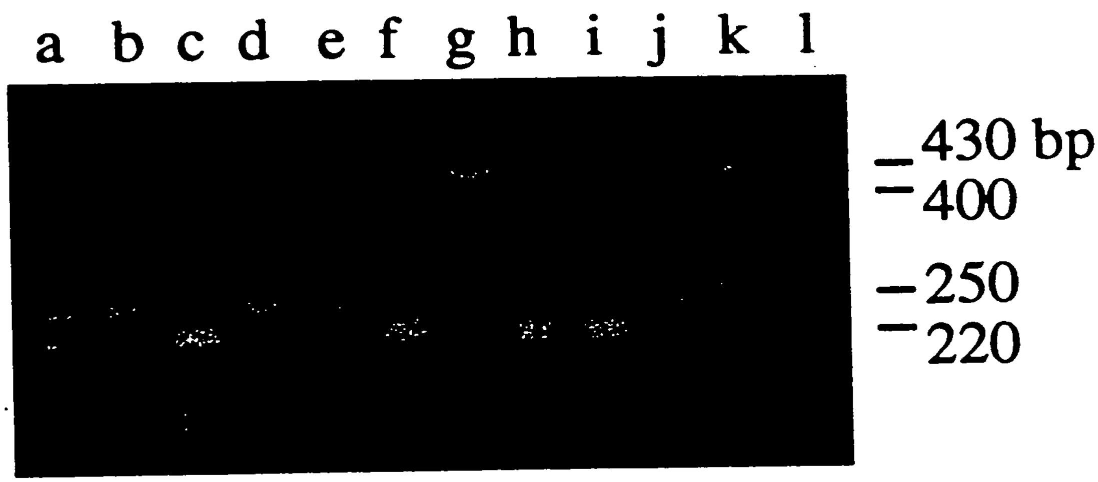

Fig. 8

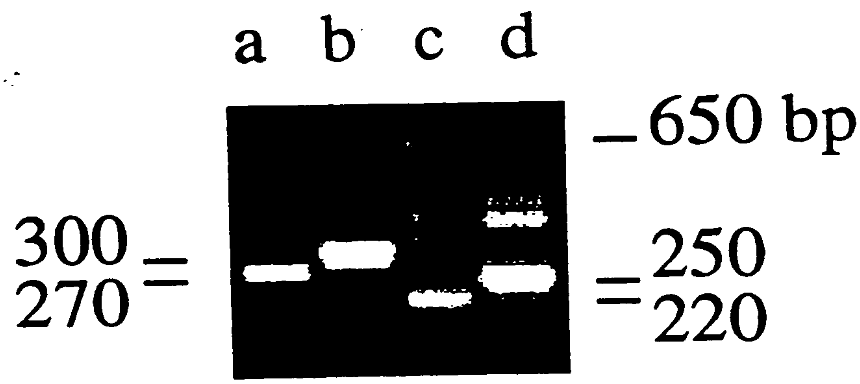

Fig. 9

sequence "Y" 104-105 bases
GGCCTCCCCGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGGCCGGGGGGAACCAG
GlyLeuProGlyValGlyValArgLeuGlyLeuArgAlaAlaGlyGlyAsnGln
AlaSerProGlySerAlaSerGlyTrpGly * GlyArgProGlyGlyThrSer
ProProArgGlyArgArgProAlaGlyValGluGlyGlyArgGlyGluProAla

CGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTG
ArgHisAlaGluSerSerAlaGlyAspSerGlyArgPheProArgArg
AspMetArgArgAlaAlaGlnAlaThrGlnGlyAlaSerProAlaGly
ThrCysGlyGluGlnArgArgArgLeuArgAlaLeuProProGlnVal

sequence "1" 38 bases
GTGGCTGTGCTTTGGTTTAACTTCCTTTTTAACCAGAA
ValAlaValLeuTrpPheAsnPheLeuPheAsnGlnLys

sequence "α" 36 bases
GTGGATGTGACGGGCGCGTACGACACCATCCCCCAG
ValAspValThrGlyAlaTyrAspThrIleProGln

sequence "β" 182 bases
GTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTG
ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu

CAGGAGACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTG
GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeu

AATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCAC
AsnGluAlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHis

GCCGTGCGCATCAGGGGCAA
AlaValArgIleArgGlyLys

partial sequence "2" unknown length
GTGAGCGCACCTGGCCGGAAGTGGAGCCTGTGCCCGGCTGGGGCAGGTGCTGCTGCAG
Ter

GGCCGTTGCGTCCACCTCTGCTTCCGTGTGGGGCAGGCGACTGCCAATCCCAAAGGGT
CAGATGCCACAGGGTGCCCCTCGTCCCATCTGGGGCTGAGCACAAATGCATCTTTCTG
TGGGAGTGAGGGTGCCTCACAACGGGAGCAGTTTTCTGTGCTATTTTGGTAA...

Fig. 10A

sequence "3" 159 bases
CCGAAGAAAACATTTCTGTCGTGACTCCTGCGGTGCTTGGGTCGGGACAGCCAGAG
AlaGluGluAsnIleSerValValThrProAlaValLeuGlySerGlyGlnProGlu

ATGGAGCCACCCCGCAGACCGTCGGGTGTGGGCAGCTTTCCGGTGTCTCCTGGGAGG
MetGluProProArgArgProSerGlyValGlySerPheProValSerProGlyArg

GGAGTTGGGCTGGGCCTGTGACTCCTCAGCCTCTGTTTTCCCCCAG
GlyValGlyLeuGlyLeu *

sequence "X" unknown length
...GACAGTCACCAGGGGGGTTGACCGCCGGACTGGGCGTCCCCAGGGTTGACTATAGGA
CCAGGTGTCCAGGTGCCCTGCAAGTAGAGGGGCTCTCAGAGGCGTCTGGCTGGCATGG
GTGGACGTGGCCCCGGGCATGGCCTTCTGCGTGTGCTGCCGTGGGTGCCCTGAGCCCT
CACTGAGTCGGTGGGGGCTTGTGGCTTCCCGTGAGCTTCCCCCTAGTCTGTTGTCTGG
CTGAGCAAGCCTCCTGAGGGGCTCTCTATTG

partial sequence of genomic intron (approximately 2.7 kb)
GTGGCTGTGCTTTGGTTTAACTTCCTTTTTAACCAGAAGTGCGTTTGAGCCCCACATT
TGGTATCAGCTTAGATGAAGGGCCCGGAGGAGGGGCCACGGGACACAGCCAGGGCCAT
GGCACGGCGCCCACCCATTTGTGCGCACAGTGAGGTGGCCGAGGTGCCGGTGCCTCCA
GAAAAGCAGCGTGGGGGTGTAGGGGGAGCTCCTGGGGCAGGGAC....

Fig. 10B

Truncated telomerase

ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTG
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCCGCCGC
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

CCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCG
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGT
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCC
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGC
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCG
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCACCACGCGGGCCCCCC
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAG
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCA
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCG
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTG
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

GACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

AAT--NNN--GACAGTCACCAGGGGGGTTGACCGCCGGACTGGGCGTCCCCAGGGTTGACTATAGGACCAGGTGTCCAGGTGCCCTGCAAGTAGAGGGGCTCTCAGAGGCGTCTGGCTGG

Fig. 11A

CATGGGTGGACGTGGCCCCGGGCATGGCCTTCTGCGTGTGCTGCCGTGGGTGCCCTGAGCCCTCACTGAGTCGGTGGGGGCTTGTGGCTTCCCGTGAGCTTCCCCCTAGTCTGTTGTCTG

GCTGAGCAAGCCTCCTGAGGGGCTCTCTATTG...

Fig. 11B

Truncated protein 1

```
ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTG
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCCGCCGC
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

CCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCG
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGT
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCC
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGC
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCG
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCACCACGCGGGCCCCCC
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAG
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCA
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCG
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTG
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

GACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G
```

Fig. 11C

AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

GTGGCTGTGCTTTGGTTTAACTTCCTTTTTAACCAGAA
V A V L W F T F L F N Q K

CGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCTCAACTACGA
G L R P I V N M D Y V V G A R T F R R E K R P S V S F R G *

Fig. 11D

Truncated protein 2

```
ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTG
M  P  R  A  P  R  C  R  A  V  R  S  L  L  R  S  H  Y  R  E  V  L  P  L  A  T  F  V

CGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCCGCCGC
R  R  L  G  P  Q  G  W  R  L  V  Q  R  G  D  P  A  A  F  R  A  L  V  A  Q  C  L  V  C  V  P  W  D  A  R  P  P  P  A  A

CCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCG
P  S  F  R  Q  V  S  C  L  K  E  L  V  A  R  V  L  Q  R  L  C  E  R  G  A  K  N  V  L  A  F  G  F  A  L  L  D  G  A  R

CGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGT
G  G  P  P  E  A  F  T  T  S  V  R  S  Y  L  P  N  T  V  T  D  A  L  R  G  S  G  A  W  G  L  L  L  R  R  V  G  D  D  V

GCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCC
L  V  H  L  L  A  R  C  A  L  F  V  L  V  A  P  S  C  A  Y  Q  V  C  G  P  P  L  Y  Q  L  G  A  A  T  Q  A  R  P  P  P

ACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGC
H  A  S  G  P  R  R  R  L  G  C  E  R  A  W  N  H  S  V  R  E  A  G  V  P  L  G  L  P  A  P  G  A  R  R  R  G  G  S  A

CAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCG
S  R  S  L  P  L  P  K  R  P  R  R  G  A  A  P  E  P  E  R  T  P  V  G  Q  G  S  W  A  H  P  G  R  T  R  G  P  S  D  R

TGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCACCACGCGGGCCCCCC
G  F  C  V  V  S  P  A  R  P  A  E  E  A  T  S  L  E  G  A  L  S  G  T  R  H  S  H  P  S  V  G  R  Q  H  H  A  G  P  P

ATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAG
S  T  S  R  P  P  R  P  W  D  T  P  C  P  P  V  Y  A  E  T  K  H  F  L  Y  S  S  G  D  K  E  Q  L  R  P  S  F  L  L  S

CTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCA
S  L  R  P  S  L  T  G  A  R  R  L  V  E  T  I  F  L  G  S  R  P  W  M  P  G  T  P  R  R  L  P  R  L  P  Q  R  Y  W  Q

AATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCG
M  R  P  L  F  L  E  L  L  G  N  H  A  Q  C  P  Y  G  V  L  L  K  T  H  C  P  L  R  A  A  V  T  P  A  A  G  V  C  A  R

GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTG
E  K  P  Q  G  S  V  A  A  P  E  E  E  D  T  D  P  R  R  L  V  Q  L  L  R  Q  H  S  S  P  W  Q  V  Y  G  F  V  R  A  C

CCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT
L  R  R  L  V  P  P  G  L  W  G  S  R  H  N  E  R  R  F  L  R  N  T  K  K  F  I  S  L  G  K  H  A  K  L  S  L  Q  E  L

GACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT
T  W  K  M  S  V  R  D  C  A  W  L  R  R  S  P  G  V  G  C  V  P  A  A  E  H  R  L  R  E  E  I  L  A  K  F  L  H  W  L

GATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
M  S  V  Y  V  V  E  L  L  R  S  F  F  Y  V  T  E  T  T  F  Q  K  N  R  L  F  F  Y  R  K  S  V  W  S  K  L  Q  S  I  G
```

Fig. 11E

```
AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA
 I  R  Q  H  L  K  R  V  Q  L  R  E  L  S  E  A  E  V  R  Q  H  R  E  A  R  P  A  L  L  T  S  R  L  R  F  I  P  K  P  D

CGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCTCAACTACGA
 G  L  R  P  I  V  N  M  D  Y  V  V  G  A  R  T  F  R  R  E  K  R  A  E  R  L  T  S  R  V  K  A  L  F  S  V  L  N  Y  E

GCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCCGCCGCCTGAGCTGTACTT
 R  A  R  R  P  G  L  L  G  A  S  V  L  G  L  D  D  I  H  R  A  W  R  T  F  V  L  R  V  R  A  Q  D  P  P  P  E  L  Y  F

TGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCGTCGGTATGCCGTGGTCCA
 V  K  V  D  V  T  G  A  Y  D  T  I  P  Q  D  R  L  T  E  V  I  A  S  I  I  K  P  Q  N  T  Y  C  V  R  R  Y  A  V  V  Q

GAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCAC
 K  A  A  H  G  H  V  R  K  A  F  K  S  H

                                                                                                        GTCCTACGTCCAGTG
                                                                                                     V  L  R  P  V

CCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCTGCTCCTGCGTTTGGTGGA
 P  G  D  P  A  G  L  H  P  L  H  A  A  L  Q  P  V  L  R  R  H  G  E  Q  A  V  C  G  D  S  A  G  R  A  A  P  A  F  G  G

TGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAAGACAGTGGTGAACTTCCC
 *
```

Fig. 11F

Reference protein

```
ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAG   60
MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu   20

GTGCTGCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAG  120
ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln   40

CGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGG  180
ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp   60

GACGCACGGCCGCCCCCCGCCGCCCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTG  240
AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu   80

GTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGC  300
ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly  100

TTCGCGCTGCTGGACGGGGCCCGCGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGC  360
PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg  120

AGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTG  420
SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu  140

TTGCGCCGCGTGGGCGACGACGTGCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTG  480
LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal  160

CTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCT  540
LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla  180

GCCACTCAGGCCCGGCCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAA  600
AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu  200

CGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGT  660
ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly  220

GCGAGGAGGCGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGT  720
AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg  240

GGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGC  780
GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly  260

AGGACGCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAA  840
ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu  280

GAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGC  900
GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly  300
```

Fig. 11G

CGCCAGCACCACGCGGGCCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCT 960
ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro 320

TGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAG 1020
CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln 340

CTGCGGCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTC 1080
LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360

GTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCC 1140
ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro 380

CGCCTGCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCAC 1200
ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis 400

GCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACC 1260
AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 420

CCAGCAGCCGGTGTCTGTGCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAG 1320
ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu 440

GAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAG 1380
GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln 460

GTGTACGGCTTCGTGCGGGCCTGCCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCC 1440
ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer 480

AGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCAT 1500
ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis 500

GCCAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTG 1560
AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu 520

CGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATC 1620
ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle 540

CTGGCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTC 1680
LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe 560

TTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTC 1740
PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580

TGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAG 1800
TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu 600

CTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGA 1860
LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620

Fig. 11H

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CTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTG   1920
LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal    640

GGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCA   1980
GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla    660

CTGTTCAGCGTGCTCAACTACGAGCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTG   2040
LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal    680

CTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAG   2100
LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln    700

GACCCGCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATC   2160
AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle    720

CCCCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGC   2220
ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys    740

GTGCGTCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAG   2280
ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys    760

AGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTG   2340
SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu    780

CAGGAGACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAG   2400
GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGlu    800

GCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATC   2460
AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle    820

AGGGGCAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTG   2520
ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu    840

CTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGAC   2580
LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp    860

GGGCTGCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCCACGCG   2640
GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla    880

AAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTG   2700
LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu    900

CGGAAGACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTT   2760
ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal    920

CAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTG   2820
GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu    940
```

Fig. 11I

GAGGTGCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTC 2880
GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960

AACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTG 2940
AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu 980

AAGTGTCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAAC 3000
LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000

ATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCA 3060
IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020

TTTCATCAGCAAGTTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCC 3120
PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAls 1040

TCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGC 3180
SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly 1060

GCCGCCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTC 3240
AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu 1080

AAGCTGACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAG 3300
LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100

ACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGCAGCCAAC 3360
ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAlaAsn 1120

CCGGCACTGCCCTCAGACTTCAAGACCATCCTGGAC 3420
ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132

Fig. 11J

Truncated protein 3

ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTG
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCCGCCGC
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

CCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCG
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGT
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCC
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGC
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCG
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCACCACGCGGGCCCCCC
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAG
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCA
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCG
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTG
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

GACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

Fig. 11K

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AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA
 I  R  Q  H  L  K  R  V  Q  L  R  E  L  S  E  A  E  V  R  Q  H  R  E  A  R  P  A  L  L  T  S  R  L  R  F  I  P  K  P  D

CGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCTCAACTACGA
 G  L  R  P  I  V  N  M  D  Y  V  V  G  A  R  T  F  R  R  E  K  R  A  E  R  L  T  S  R  V  K  A  L  F  S  V  L  N  Y  E

GCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCCGCCGCCTGAGCTGTACTT
 R  A  R  R  P  G  L  L  G  A  S  V  L  G  L  D  D  I  H  R  A  W  R  T  F  V  L  R  V  R  A  Q  D  P  P  P  E  L  Y  F

TGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCGTCGGTATGCCGTGGTCCA
 V  K  V  D  V  T  G  A  Y  D  T  I  P  Q  D  R  L  T  E  V  I  A  S  I  I  K  P  Q  N  T  Y  C  V  R  R  Y  A  V  V  Q

GAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGACCAGCCCGCTGAGGGA
 K  A  A  H  G  H  V  R  K  A  F  K  S  H  V  S  T  L  T  D  L  Q  P  Y  M  R  Q  F  V  A  H  L  Q  E  T  S  P  L  R  D

TGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGTCCTACGTCCAGTG
 A  V  V  I  E  Q  S  S  S  L  N  E  A  S  S  G  L  F  D  V  F  L  R  F  M  C  H  H  A  V  R  I  R  G  K  S  Y  V  Q  C

CCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCTGCTCCTGCGTTTGGTGGA
 Q  G  I  P  Q  G  S  I  L  S  T  L  L  C  S  L  C  Y  G  D  M  E  N  K  L  F  A  G  I  R  R  D  G  L  L  L  R  L  V  D

TGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAAGACAGTGGTGAACTTCCC
 D  F  L  L  V  T  P  H  L  T  H  A  K  T  F  L  R  T  L  V  R  G  V  P  E  Y  G  C  V  V  N  L  R  K  T  V  V  N  F  P

TGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCGACTACTCCAG
 V  E  D  E  A  L  G  G  T  A  F  V  Q  M  P  A  H  G  L  F  P  W  C  G  L  L  L  D  T  R  T  L  E  V  Q  S  D  Y  S  R

GTGAGCGCACCTGGCCGGAAGTGGAGCCTGTGCCCGGCTGGGGCAGGTGCTGCTGCAGGGCCGTTGCGTCCACCTCTGCTTCCGTGTGGGGCAGGCGACTGCCAATCCCAAAGGGTCAGA
 *

TGCCACAGGGTGCCCCTCGTCCCATCTGGGGCTGAGCACAAATGCATCTTTCTGTGGGAGTGAGGGTGCCTCACAACGGGAGCAGTTTTCTGTGCTATTTTGGTAA.....
```

Fig. 11L

Altered C-terminus protein

ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTG
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCCGCCGC
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

CCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCG
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGT
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCC
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGC
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCG
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCACCACGCGGGCCCCCC
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAG
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCA
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCG
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTG
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

GACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

Fig. 11M

AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

CGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCTCAACTACGA
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E

GCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCCGCCGCCTGAGCTGTACTT
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F

TGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCGTCGGTATGCCGTGGTCCA
V K V D V T G A Y D T I P Q D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q

GAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGACCAGCCCGCTGAGGGA
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D

TGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGTCCTACGTCCAGTG
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C

CCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCTGCTCCTGCGTTTGGTGGA
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D

TGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAAGACAGTGGTGAACTTCCC
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P

TGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCGACTACTCCAG
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S S

CTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTCACAGCCTGTTTCTGGA
Y A R T S I R A S L T F N R G F K A G R N M R R K L F G V L R L K C H S L F L D

TTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCATCAGCAAGTTTGGAAGAA
L Q V N S L Q T V C T N I Y K I L L L Q A Y R F H A C V L Q L P F H Q Q V W K N

CCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGCGCCGCCGGCCCTCTGCCCTCCGA
P T F F L R V I S D T A S L C Y S I L K A K N A E

CCGAAGAAAACATTTCTGTCGTGACTCCTGCGGTGCTTGGGTC
E E N I L V V T P A V L G S

GGGACAGCCAGAGATGGAGCCACCCCGCAGACCGTCGGGTGTGGGCAGCTTTCCGGTGTCTCCTGGGAGGGGAGTTGGGCTGGGCCTGTGACTCCTCAGCCTCTGTTTTCCCCCAG
G Q P E M E P P R R P S G V G S F P V S P G R G V G L G L *

Fig. 11N

Protein that lacks motif A

ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTG
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCCGCCGC
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

CCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCG
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGT
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCC
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGC
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCG
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCACCACGCGGGCCCCCC
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAG
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCA
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCG
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTG
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

GACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

Fig. 11O

AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

CGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCTCAACTACGA
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E

GCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCCGCCGCCTGAGCTGTACTT
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F

TGTCAAG GACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCGTCGGTATGCCGTGGTCCA
V K D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q

GAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGACCAGCCCGCTGAGGGA
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D

TGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGTCCTACGTCCAGTG
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C

CCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCTGCTCCTGCGTTTGGTGGA
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D

TGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAAGACAGTGGTGAACTTCCC
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P

TGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCGACTACTCCAG
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S S

CTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTCACAGCCTGTTTCTGGA
Y A R T S I R A S L T F N R G F K A G R N M R R K L F G V L R L K C H S L F L D

TTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCATCAGCAAGTTTGGAAGAA
L Q V N S L Q T V C T N I Y K I L L L Q A Y R F H A C V L Q L P F H Q Q V W K N

CCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGCGCCGCCGGCCCTCTGCCCTCCGA
P T F F L R V I S D T A S L C Y S I L K A K N A G M S L G A K G A A G P L P S E

GGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCTGACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCAGCTGAGTCGGAAGCTCCC
A V Q W L C H Q A F L L K L T R H R V T Y V P L L G S L R T A Q T Q L S R K L P

GGGGACGACGCTGACTGCCCTGGAGGCCGCAGCCAACCCGGCACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCACAGCCAGGCCGAGAGCAGACACCAGCAGCC
G T T L T A L E A A A N P A L P S D F K T I L D

CTGTCACGCCGGGCTCTACGTCCCAGGGAGGGAGGGGCGGCCCACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCT

GAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCAGGGCCAGCTTTTCCTCAC

CAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGATTCGCCATTGTTCACCCCTCGCCCTGCCCTCCTTTGCCTTCCACCCCCACCATCCAGGTGGAGACCCTGAGAA

Fig. 11P

GGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAA

AATACTGAATATATGAGTTTTTCAGTTTTGA

Fig. 11Q

Truncated protein that lacks motif A

```
ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTG
M  P  R  A  P  R  C  R  A  V  R  S  L  L  R  S  H  Y  R  E  V  L  P  L  A  T  F  V

CGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCCGCCGC
R  R  L  G  P  Q  G  W  R  L  V  Q  R  G  D  P  A  A  F  R  A  L  V  A  Q  C  L  V  C  V  P  W  D  A  R  P  P  P  A  A

CCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCG
P  S  F  R  Q  V  S  C  L  K  E  L  V  A  R  V  L  Q  R  L  C  E  R  G  A  K  N  V  L  A  F  G  F  A  L  L  D  G  A  R

CGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGT
G  G  P  P  E  A  F  T  T  S  V  R  S  Y  L  P  N  T  V  T  D  A  L  R  G  S  G  A  W  G  L  L  L  R  R  V  G  D  D  V

GCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCC
L  V  H  L  L  A  R  C  A  L  F  V  L  V  A  P  S  C  A  Y  Q  V  C  G  P  P  L  Y  Q  L  G  A  A  T  Q  A  R  P  P  P

ACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGC
H  A  S  G  P  R  R  R  L  G  C  E  R  A  W  N  H  S  V  R  E  A  G  V  P  L  G  L  P  A  P  G  A  R  R  R  G  G  S  A

CAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCG
S  R  S  L  P  L  P  K  R  P  R  R  G  A  A  P  E  P  E  R  T  P  V  G  Q  G  S  W  A  H  P  G  R  T  R  G  P  S  D  R

TGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCACCACGCGGGCCCCCC
G  F  C  V  V  S  P  A  R  P  A  E  E  A  T  S  L  E  G  A  L  S  G  T  R  H  S  H  P  S  V  G  R  Q  H  H  A  G  P  P

ATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAG
S  T  S  R  P  P  R  P  W  D  T  P  C  P  P  V  Y  A  E  T  K  H  F  L  Y  S  S  G  D  K  E  Q  L  R  P  S  F  L  L  S

CTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCA
S  L  R  P  S  L  T  G  A  R  R  L  V  E  T  I  F  L  G  S  R  P  W  M  P  G  T  P  R  R  L  P  R  L  P  Q  R  Y  W  Q

AATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCG
M  R  P  L  F  L  E  L  L  G  N  H  A  Q  C  P  Y  G  V  L  L  K  T  H  C  P  L  R  A  A  V  T  P  A  A  G  V  C  A  R

GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTG
E  K  P  Q  G  S  V  A  A  P  E  E  E  D  T  D  P  R  R  L  V  Q  L  L  R  Q  H  S  S  P  W  Q  V  Y  G  F  V  R  A  C

CCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT
L  R  R  L  V  P  P  G  L  W  G  S  R  H  N  E  R  R  F  L  R  N  T  K  K  F  I  S  L  G  K  H  A  K  L  S  L  Q  E  L

GACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT
T  W  K  M  S  V  R  D  C  A  W  L  R  R  S  P  G  V  G  C  V  P  A  A  E  H  R  L  R  E  E  I  L  A  K  F  L  H  W  L

GATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
M  S  V  Y  V  V  E  L  L  R  S  F  F  Y  V  T  E  T  T  F  Q  K  N  R  L  F  F  Y  R  K  S  V  W  S  K  L  Q  S  I  G
```

Fig. 11R

AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

CGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCTCAACTACGA
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E

GCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCCGCCGCCTGAGCTGTACTT
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F

TGTCAAG GACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCGTCGGTATGCCGTGGTCCA
V K D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q

GAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGACCAGCCCGCTGAGGGA
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D

TGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGTCCTACGTCCAGTG
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C

CCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCTGCTCCTGCGTTTGGTGGA
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D

TGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAAGACAGTGGTGAACTTCCC
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P

TGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCGACTACTCCAG
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S R

GTGAGCGCACCTGGCCGGAAGTGGAGCCTGTGCCCGGCTGGGGCAGGTGCTGCTGCAGGGCCGTTGCGTCCACCTCTGCTTCCGTGTGGGGCAGGCGACTGCCAATCCCAAAGGGTCAGA
*

TGCCACAGGGTGCCCCTCGTCCCATCTGGGGCTGAGCACAAATGCATCTTTCTGTGGGAGTGAGGGTGCCTCACAACGGGAGCAGTTTTCTGTGCTATTTTGGTAA....

Fig. 11S

Lacks motif A and altered C-terminus

ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTG
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCCGCCGC
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

CCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCG
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGT
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCC
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGC
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCG
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCACCACGCGGGCCCCCC
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAG
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCA
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCG
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTG
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

GACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

Fig. 11T

AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

CGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCTCAACTACGA
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E

GCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCCGCCGCCTGAGCTGTACTT
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F

TGTCAAG GACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCGTCGGTATGCCGTGGTCCA
V K D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q

GAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGACCAGCCCGCTGAGGGA
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D

TGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGTCCTACGTCCAGTG
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C

CCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCTGCTCCTGCGTTTGGTGGA
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D

TGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAAGACAGTGGTGAACTTCCC
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P

TGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCGACTACTCCAG
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S S

CTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTCACAGCCTGTTTCTGGA
Y A R T S I R A S L T F N R G F K A G R N M R R K L F G V L R L K C H S L F L D

TTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCATCAGCAAGTTTGGAAGAA
L Q V N S L Q T V C T N I Y K I L L L Q A Y R F H A C V L Q L P F H Q Q V W K N

CCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGCGCCGCCGGCCCTCTGCCCTCCGA
P T F F L R V I S D T A S L C Y S I L K A K N A E

|
CCGAAGAAAACATTTCTGTCGTGACTCCTGCGGTGCTTGGGTC
E E N I L V V T P A V L G S

GGGACAGCCAGAGATGGAGCCACCCCGCAGACCGTCGGGTGTGGGCAGCTTTCCGGTGTCTCCTGGGAGGGGAGTTGGGCTGGGCCTGTGACTCCTCAGCCTCTGTTTTCCCCCAG
G Q P E M E P P R R P S G V G S F P V S P G R G V G L G L *

Fig. 11U

Truncated telomerase (ver. 2)

ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTG

M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCCGCCGC

R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

GGCCTCCCCGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGGCCGGGGGGAACCAGCGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTG

G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R

A S P G S A S G W G * G R P G G T S D M R R A A Q A T Q G A S P A G

P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V

CCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCG

P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGT

G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCC

L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGC

H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCG

S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCACCACGCGGGCCCCCC

G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAG

S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCA

S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCG

M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTG

E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT

L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

Fig. 11V

```
GACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT
 T  W  K  M  S  V  R  D  C  A  W  L  R  R  S  P  G  V  G  C  V  P  A  A  E  H  R  L  R  E  E  I  L  A  K  F  L  H  W  L

GATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
 M  S  V  Y  V  V  E  L  L  R  S  F  F  Y  V  T  E  T  T  F  Q  K  N  R  L  F  F  Y  R  K  S  V  W  S  K  L  Q  S  I  G

AAT--NNN--GACAGTCACCAGGGGGGTTGACCGCCGGACTGGGCGTCCCCAGGGTTGACTATAGGACCAGGTGTCCAGGTGCCCTGCAAGTAGAGGGGCTCTCAGAGGCGTCTGGCTGG

CATGGGTGGACGTGGCCCCGGGCATGGCCTTCTGCGTGTGCTGCCGTGGGTGCCCTGAGCCCTCACTGAGTCGGTGGGGGCTTGTGGCTTCCCGTGAGCTTCCCCCTAGTCTGTTGTCTG

GCTGAGCAAGCCTCCTGAGGGGCTCTCTATTG...
```

Fig. 11W

Truncated protein 1 (ver. 2)

```
ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTG
M  P  R  A  P  R  C  R  A  V  R  S  L  L  R  S  H  Y  R  E  V  L  P  L  A  T  F  V

CGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCCGCCGC
R  R  L  G  P  Q  G  W  R  L  V  Q  R  G  D  P  A  A  F  R  A  L  V  A  Q  C  L  V  C  V  P  W  D  A  R  P  P  P  A  A

GGCCTCCCCGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGGCCGGGGGGAACCAGCGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTG
G  L  P  G  V  G  V  R  L  G  L  R  A  A  G  G  N  Q  R  H  A  E  S  S  A  G  D  S  G  R  F  P  R  R
 A  S  P  G  S  A  S  G  W  G  *  G  R  P  G  G  T  S  D  M  R  R  A  A  Q  A  T  Q  G  A  S  P  A  G
  P  P  R  G  R  R  P  A  G  V  E  G  G  R  G  E  P  A  T  C  G  E  Q  R  R  R  L  R  A  L  P  P  Q  V

CCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCG
P  S  F  R  Q  V  S  C  L  K  E  L  V  A  R  V  L  Q  R  L  C  E  R  G  A  K  N  V  L  A  F  G  F  A  L  L  D  G  A  R

CGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGT
G  G  P  P  E  A  F  T  T  S  V  R  S  Y  L  P  N  T  V  T  D  A  L  R  G  S  G  A  W  G  L  L  L  R  R  V  G  D  D  V

GCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCC
L  V  H  L  L  A  R  C  A  L  F  V  L  V  A  P  S  C  A  Y  Q  V  C  G  P  P  L  Y  Q  L  G  A  A  T  Q  A  R  P  P  P

ACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGC
H  A  S  G  P  R  R  R  L  G  C  E  R  A  W  N  H  S  V  R  E  A  G  V  P  L  G  L  P  A  P  G  A  R  R  R  G  G  S  A

CAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCG
S  R  S  L  P  L  P  K  R  P  R  R  G  A  A  P  E  P  E  R  T  P  V  G  Q  G  S  W  A  H  P  G  R  T  R  G  P  S  D  R

TGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCACCACGCGGGCCCCCC
G  F  C  V  V  S  P  A  R  P  A  E  E  A  T  S  L  E  G  A  L  S  G  T  R  H  S  H  P  S  V  G  R  Q  H  H  A  G  P  P

ATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAG
S  T  S  R  P  P  R  P  W  D  T  P  C  P  P  V  Y  A  E  T  K  H  F  L  Y  S  S  G  D  K  E  Q  L  R  P  S  F  L  L  S

CTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCA
S  L  R  P  S  L  T  G  A  R  R  L  V  E  T  I  F  L  G  S  R  P  W  M  P  G  T  P  R  R  L  P  R  L  P  Q  R  Y  W  Q

AATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCG
M  R  P  L  F  L  E  L  L  G  N  H  A  Q  C  P  Y  G  V  L  L  K  T  H  C  P  L  R  A  A  V  T  P  A  A  G  V  C  A  R

GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTG
E  K  P  Q  G  S  V  A  A  P  E  E  E  D  T  D  P  R  R  L  V  Q  L  L  R  Q  H  S  S  P  W  Q  V  Y  G  F  V  R  A  C

CCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT
L  R  R  L  V  P  P  G  L  W  G  S  R  H  N  E  R  R  F  L  R  N  T  K  K  F  I  S  L  G  K  H  A  K  L  S  L  Q  E  L
```

Fig. 11X

```
GACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT
 T  W  K  M  S  V  R  D  C  A  W  L  R  R  S  P  G  V  G  C  V  P  A  A  E  H  R  L  R  E  E  I  L  A  K  F  L  H  W  L

GATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
 M  S  V  Y  V  V  E  L  L  R  S  F  F  Y  V  T  E  T  T  F  Q  K  N  R  L  F  F  Y  R  K  S  V  W  S  K  L  Q  S  I  G

AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA
 I  R  Q  H  L  K  R  V  Q  L  R  E  L  S  E  A  E  V  R  Q  H  R  E  A  R  P  A  L  L  T  S  R  L  R  F  I  P  K  P  D

                                                                      GTGGCTGTGCTTTGGTTTAACTTCCTTTTTAACCAGAA
                                                                       V  A  V  L  W  F  T  F  L  F  N  Q  K
                                                                     |
CGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCTCAACTACGA
 G  L  R  P  I  V  N  M  D  Y  V  V  G  A  R  T  F  R  R  E  K  R  P  S  V  S  F  R  G  *
```

Fig. 11Y

Truncated protein 2 (ver. 2)

ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTG
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCCGCCGC
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

GGCCTCCCCGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGGCCGGGGGGAACCAGCGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTG
G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R
A S P G S A S G W G * G R P G G T S D M R R A A Q A T Q G A S P A G
P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V

CCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCG
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGT
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCC
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGC
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCG
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCACCACGCGGGCCCCCC
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAG
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCA
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCG
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTG
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

Fig. 11Z

```
GACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT
 T  W  K  M  S  V  R  D  C  A  W  L  R  R  S  P  G  V  G  C  V  P  A  A  E  H  R  L  R  E  E  I  L  A  K  F  L  H  W  L

GATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
 M  S  V  Y  V  V  E  L  L  R  S  F  F  Y  V  T  E  T  T  F  Q  K  N  R  L  F  F  Y  R  K  S  V  W  S  K  L  Q  S  I  G

AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA
 I  R  Q  H  L  K  R  V  Q  L  R  E  L  S  E  A  E  V  R  Q  H  R  E  A  R  P  A  L  L  T  S  R  L  R  F  I  P  K  P  D

CGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCTCAACTACGA
 G  L  R  P  I  V  N  M  D  Y  V  V  G  A  R  T  F  R  R  E  K  R  A  E  R  L  T  S  R  V  K  A  L  F  S  V  L  N  Y  E

GCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCCGCCGCCTGAGCTGTACTT
 R  A  R  R  P  G  L  L  G  A  S  V  L  G  L  D  D  I  H  R  A  W  R  T  F  V  L  R  V  R  A  Q  D  P  P  P  E  L  Y  F

TGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCGTCGGTATGCCGTGGTCCA
 V  K  V  D  V  T  G  A  Y  D  T  I  P  Q  D  R  L  T  E  V  I  A  S  I  I  K  P  Q  N  T  Y  C  V  R  R  Y  A  V  V  Q

GAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCAC
 K  A  A  H  G  H  V  R  K  A  F  K  S  H

                                                                                                           GTCCTACGTCCAGTG
                                                                                                 V  L  R  P  V

CCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCTGCTCCTGCGTTTGGTGGA
 P  G  D  P  A  G  L  H  P  L  H  A  A  L  Q  P  V  L  R  R  H  G  E  Q  A  V  C  G  D  S  A  G  R  A  A  P  A  F  G  G

TGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAAGACAGTGGTGAACTTCCC
 *
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Fig. 11AA

Reference protein (ver. 2)

ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAG 60
MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 20

GTGCTGCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAG 120
ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln 40

CGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGG 180
ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp 60

GACGCACGGCCGCCCCCCGCCGCCCCCTCCTTCCGCCAGGTG
AspAlaArgProProProAlaAlaProSerPheArgGlnVal

GGCCTCCCCGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGGCCGGGGGGAACCAGCGACATGCGGAG
G L P G V G V R L G L R A A G G N Q R H A E
A S P G S A S G W G * G R P G G T S D M R R
P P R G R R P A G V E G G R G E P A T C G E

AGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTG
S S A G D S G R F P R R
A A Q A T Q G A S P A G
Q R R R L R A L P P Q V

TCCTGCCTGAAGGAGCTG 240
SerCysLeuLysGluLeu 80

GTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGC 300
ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly 100

TTCGCGCTGCTGGACGGGGCCCGCGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGC 360
PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg 120

AGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTG 420
SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu 140

TTGCGCCGCGTGGGCGACGACGTGCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTG 480
LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160

CTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCT 540
LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180

GCCACTCAGGCCCGGCCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAA 600
AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200

Fig. 11AB

```
CGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCTGGGCCTGCCAGCCCCGGGT     660
ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly     220

GCGAGGAGGCGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGT     720
AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg     240

GGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGC     780
GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly     260

AGGACGCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAA     840
ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu     280

GAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGC     900
GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly     300

CGCCAGCACCACGCGGGCCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCT     960
ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro     320

TGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAG    1020
CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln     340

CTGCGGCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTC    1080
LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu     360

GTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCC    1140
ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro     380

CGCCTGCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCAC    1200
ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis     400

GCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACC    1260
AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr     420

CCAGCAGCCGGTGTCTGTGCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAG    1320
ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu     440

GAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAG    1380
GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln     460

GTGTACGGCTTCGTGCGGGCCTGCCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCC    1440
ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer     480

AGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCAT    1500
ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis     500

GCCAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGGCTGCGCTTGGCTG    1560
AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu     520
```

Fig. 11AC

CGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATC 1620
ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle 540

CTGGCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTC 1680
LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe 560

TTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTC 1740
PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580

TGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAG 1800
TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu 600

CTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGA 1860
LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620

CTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTG 1920
LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640

GGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCA 1980
GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla 660

CTGTTCAGCGTGCTCAACTACGAGCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTG 2040
LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680

CTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAG 2100
LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln 700

GACCCGCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATC 2160
AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle 720

CCCCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGC 2220
ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys 740

GTGCGTCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAG 2280
ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys 760

AGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTG 2340
SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780

CAGGAGACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAG 2400
GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGlu 800

GCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATC 2460
AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle 820

AGGGGCAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTG 2520
ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840

Fig. 11AD

CTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGAC 2580
LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp 860

GGGCTGCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCCACGCG 2640
GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880

AAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTG 2700
LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 900

CGGAAGACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTT 2760
ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 920

CAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTG 2820
GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu 940

GAGGTGCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTC 2880
GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960

AACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTG 2940
AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu 980

AAGTGTCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAAC 3000
LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000

ATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCA 3060
IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020

TTTCATCAGCAAGTTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCC 3120
PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAls 1040

TCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGC 3180
SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly 1060

GCCGCCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTC 3240
AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu 1080

AAGCTGACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAG 3300
LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100

ACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGCAGCCAAC 3360
ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAlaAsn 1120

CCGGCACTGCCCTCAGACTTCAAGACCATCCTGGAC 3420
ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132

Fig. 11AE

Truncated protein 3 (ver. 2)

```
                                   ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTG
                                   M  P  R  A  P  R  C  R  A  V  R  S  L  L  R  S  H  Y  R  E  V  L  P  L  A  T  F  V

CGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCCGCCGC
R  R  L  G  P  Q  G  W  R  L  V  Q  R  G  D  P  A  A  F  R  A  L  V  A  Q  C  L  V  C  V  P  W  D  A  R  P  P  P  A  A

                   GGCCTCCCCGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGGCCGGGGGGAACCAGCGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTG
                   G  L  P  G  V  G  V  R  L  G  L  R  A  A  G  G  N  Q  R  H  A  E  S  S  A  G  D  S  G  R  F  P  R  R
                    A  S  P  G  S  A  S  G  W  G  *  G  R  P  G  G  T  S  D  M  R  R  A  A  Q  A  T  Q  G  A  S  P  A  G
                     P  P  R  G  R  R  P  A  G  V  E  G  G  R  G  E  P  A  T  C  G  E  Q  R  R  R  L  R  A  L  P  P  Q  V
                   |
CCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCG
P  S  F  R  Q  V  S  C  L  K  E  L  V  A  R  V  L  Q  R  L  C  E  R  G  A  K  N  V  L  A  F  G  F  A  L  L  D  G  A  R

CGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGT
G  G  P  P  E  A  F  T  T  S  V  R  S  Y  L  P  N  T  V  T  D  A  L  R  G  S  G  A  W  G  L  L  L  R  R  V  G  D  D  V

GCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCC
L  V  H  L  L  A  R  C  A  L  F  V  L  V  A  P  S  C  A  Y  Q  V  C  G  P  P  L  Y  Q  L  G  A  A  T  Q  A  R  P  P  P

ACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGC
H  A  S  G  P  R  R  R  L  G  C  E  R  A  W  N  H  S  V  R  E  A  G  V  P  L  G  L  P  A  P  G  A  R  R  R  G  G  S  A

CAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCG
S  R  S  L  P  L  P  K  R  P  R  R  G  A  A  P  E  P  E  R  T  P  V  G  Q  G  S  W  A  H  P  G  R  T  R  G  P  S  D  R

TGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCACCACGCGGGCCCCCC
G  F  C  V  V  S  P  A  R  P  A  E  E  A  T  S  L  E  G  A  L  S  G  T  R  H  S  H  P  S  V  G  R  Q  H  H  A  G  P  P

ATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAG
S  T  S  R  P  P  R  P  W  D  T  P  C  P  P  V  Y  A  E  T  K  H  F  L  Y  S  S  G  D  K  E  Q  L  R  P  S  F  L  L  S

CTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCA
S  L  R  P  S  L  T  G  A  R  R  L  V  E  T  I  F  L  G  S  R  P  W  M  P  G  T  P  R  R  L  P  R  L  P  Q  R  Y  W  Q

AATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCG
M  R  P  L  F  L  E  L  L  G  N  H  A  Q  C  P  Y  G  V  L  L  K  T  H  C  P  L  R  A  A  V  T  P  A  A  G  V  C  A  R

GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTG
E  K  P  Q  G  S  V  A  A  P  E  E  E  D  T  D  P  R  R  L  V  Q  L  L  R  Q  H  S  S  P  W  Q  V  Y  G  F  V  R  A  C

CCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT
L  R  R  L  V  P  P  G  L  W  G  S  R  H  N  E  R  R  F  L  R  N  T  K  K  F  I  S  L  G  K  H  A  K  L  S  L  Q  E  L
```

Fig. 11AF

GACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

CGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCTCAACTACGA
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E

GCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCCGCCGCCTGAGCTGTACTT
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F

TGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCGTCGGTATGCCGTGGTCCA
V K V D V T G A Y D T I P Q D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q

GAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGACCAGCCCGCTGAGGGA
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D

TGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGTCCTACGTCCAGTG
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C

CCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCTGCTCCTGCGTTTGGTGGA
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D

TGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAAGACAGTGGTGAACTTCCC
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P

TGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCGACTACTCCAG
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S R

GTGAGCGCACCTGGCCGGAAGTGGAGCCTGTGCCCGGCTGGGGCAGGTGCTGCTGCAGGGCCGTTGCGTCCACCTCTGCTTCCGTGTGGGGCAGGCGACTGCCAATCCCAAAGGGTCAGA
*

TGCCACAGGGTGCCCCTCGTCCCATCTGGGGCTGAGCACAAATGCATCTTTCTGTGGGAGTGAGGGTGCCTCACAACGGGAGCAGTTTTCTGTGCTATTTTGGTAA.....

Fig. 11AG

Altered C-terminus protein (ver. 2)

```
                                          ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTG
                                          M  P  R  A  P  R  C  R  A  V  R  S  L  L  R  S  H  Y  R  E  V  L  P  L  A  T  F  V

CGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCCGCCGC
R  R  L  G  P  Q  G  W  R  L  V  Q  R  G  D  P  A  A  F  R  A  L  V  A  Q  C  L  V  C  V  P  W  D  A  R  P  P  P  A  A

            GGCCTCCCCGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGGCCGGGGGGAACCAGCGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTG
            G  L  P  G  V  G  V  R  L  G  L  R  A  A  G  G  N  Q  R  H  A  E  S  S  A  G  D  S  G  R  F  P  R  R
             A  S  P  G  S  A  S  G  W  G  *  G  R  P  G  G  T  S  D  M  R  R  A  A  Q  A  T  Q  G  A  S  P  A  G
              P  P  R  G  R  R  P  A  G  V  E  G  G  R  G  E  P  A  T  C  G  E  Q  R  R  R  L  R  A  L  P  P  Q  V
            |
CCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCG
P  S  F  R  Q  V  S  C  L  K  E  L  V  A  R  V  L  Q  R  L  C  E  R  G  A  K  N  V  L  A  F  G  F  A  L  L  D  G  A  R

CGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGT
G  G  P  P  E  A  F  T  T  S  V  R  S  Y  L  P  N  T  V  T  D  A  L  R  G  S  G  A  W  G  L  L  L  R  R  V  G  D  D  V

GCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCC
L  V  H  L  L  A  R  C  A  L  F  V  L  V  A  P  S  C  A  Y  Q  V  C  G  P  P  L  Y  Q  L  G  A  A  T  Q  A  R  P  P  P

ACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGC
H  A  S  G  P  R  R  R  L  G  C  E  R  A  W  N  H  S  V  R  E  A  G  V  P  L  G  L  P  A  P  G  A  R  R  R  G  G  S  A

CAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCG
S  R  S  L  P  L  P  K  R  P  R  R  G  A  A  P  E  P  E  R  T  P  V  G  Q  G  S  W  A  H  P  G  R  T  R  G  P  S  D  R

TGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCACCACGCGGGCCCCCC
G  F  C  V  V  S  P  A  R  P  A  E  E  A  T  S  L  E  G  A  L  S  G  T  R  H  S  H  P  S  V  G  R  Q  H  H  A  G  P  P

ATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAG
S  T  S  R  P  P  R  P  W  D  T  P  C  P  P  V  Y  A  E  T  K  H  F  L  Y  S  S  G  D  K  E  Q  L  R  P  S  F  L  L  S

CTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCA
S  L  R  P  S  L  T  G  A  R  R  L  V  E  T  I  F  L  G  S  R  P  W  M  P  G  T  P  R  R  L  P  R  L  P  Q  R  Y  W  Q

AATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCG
M  R  P  L  F  L  E  L  L  G  N  H  A  Q  C  P  Y  G  V  L  L  K  T  H  C  P  L  R  A  A  V  T  P  A  A  G  V  C  A  R

GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTG
E  K  P  Q  G  S  V  A  A  P  E  E  E  D  T  D  P  R  R  L  V  Q  L  L  R  Q  H  S  S  P  W  Q  V  Y  G  F  V  R  A  C

CCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT
L  R  R  L  V  P  P  G  L  W  G  S  R  H  N  E  R  R  F  L  R  N  T  K  K  F  I  S  L  G  K  H  A  K  L  S  L  Q  E  L
```

Fig. 11AH

GACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT

T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG

M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA

I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

CGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCTCAACTACGA

G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E

GCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCCGCCGCCTGAGCTGTACTT

R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F

TGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCGTCGGTATGCCGTGGTCCA

V K V D V T G A Y D T I P Q D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q

GAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGACCAGCCCGCTGAGGGA

K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D

TGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGTCCTACGTCCAGTG

A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C

CCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCTGCTCCTGCGTTTGGTGGA

Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D

TGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAAGACAGTGGTGAACTTCCC

D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P

TGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCGACTACTCCAG

V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S S

CTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTCACAGCCTGTTTCTGGA

Y A R T S I R A S L T F N R G F K A G R N M R R K L F G V L R L K C H S L F L D

TTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCATCAGCAAGTTTGGAAGAA

L Q V N S L Q T V C T N I Y K I L L L Q A Y R F H A C V L Q L P F H Q Q V W K N

CCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGCGCCGCCGGCCCTCTGCCCTCCGA

P T F F L R V I S D T A S L C Y S I L K A K N A E

CCGAAGAAAACATTTCTGTCGTGACTCCTGCGGTGCTTGGGTC

E E N I L V V T P A V L G S

GGGACAGCCAGAGATGGAGCCACCCCGCAGACCGTCGGGTGTGGGCAGCTTTCCGGTGTCTCCTGGGAGGGGAGTTGGGCTGGGCCTGTGACTCCTCAGCCTCTGTTTTCCCCCAG

G Q P E M E P P R R P S G V G S F P V S P G R G V G L G L *

Fig. 11AI

Protein that lacks motif A (ver. 2)

```
ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTG
 M  P  R  A  P  R  C  R  A  V  R  S  L  L  R  S  H  Y  R  E  V  L  P  L  A  T  F  V

CGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCCGCCGC
 R  R  L  G  P  Q  G  W  R  L  V  Q  R  G  D  P  A  A  F  R  A  L  V  A  Q  C  L  V  C  V  P  W  D  A  R  P  P  P  A  A

GGCCTCCCCGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGGCCGGGGGGAACCAGCGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTG
 G  L  P  G  V  G  V  R  L  G  L  R  A  A  G  G  N  Q  R  H  A  E  S  S  A  G  D  S  G  R  F  P  R  R
  A  S  P  G  S  A  S  G  W  G  *  G  R  P  G  G  T  S  D  M  R  R  A  A  Q  A  T  Q  G  A  S  P  A  G
   P  P  R  G  R  R  P  A  G  V  E  G  G  R  G  E  P  A  T  C  G  E  Q  R  R  R  L  R  A  L  P  P  Q  V

CCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCG
 P  S  F  R  Q  V  S  C  L  K  E  L  V  A  R  V  L  Q  R  L  C  E  R  G  A  K  N  V  L  A  F  G  F  A  L  L  D  G  A  R

CGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGT
 G  G  P  P  E  A  F  T  T  S  V  R  S  Y  L  P  N  T  V  T  D  A  L  R  G  S  G  A  W  G  L  L  L  R  R  V  G  D  D  V

GCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCC
 L  V  H  L  L  A  R  C  A  L  F  V  L  V  A  P  S  C  A  Y  Q  V  C  G  P  P  L  Y  Q  L  G  A  A  T  Q  A  R  P  P  P

ACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGC
 H  A  S  G  P  R  R  R  L  G  C  E  R  A  W  N  H  S  V  R  E  A  G  V  P  L  G  L  P  A  P  G  A  R  R  R  G  G  S  A

CAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCG
 S  R  S  L  P  L  P  K  R  P  R  R  G  A  A  P  E  P  E  R  T  P  V  G  Q  G  S  W  A  H  P  G  R  T  R  G  P  S  D  R

TGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCACCACGCGGGCCCCCC
 G  F  C  V  V  S  P  A  R  P  A  E  E  A  T  S  L  E  G  A  L  S  G  T  R  H  S  H  P  S  V  G  R  Q  H  H  A  G  P  P

ATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAG
 S  T  S  R  P  P  R  P  W  D  T  P  C  P  P  V  Y  A  E  T  K  H  F  L  Y  S  S  G  D  K  E  Q  L  R  P  S  F  L  L  S

CTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCA
 S  L  R  P  S  L  T  G  A  R  R  L  V  E  T  I  F  L  G  S  R  P  W  M  P  G  T  P  R  R  L  P  R  L  P  Q  R  Y  W  Q

AATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCG
 M  R  P  L  F  L  E  L  L  G  N  H  A  Q  C  P  Y  G  V  L  L  K  T  H  C  P  L  R  A  A  V  T  P  A  A  G  V  C  A  R

GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTG
 E  K  P  Q  G  S  V  A  A  P  E  E  E  D  T  D  P  R  R  L  V  Q  L  L  R  Q  H  S  S  P  W  Q  V  Y  G  F  V  R  A  C

CCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT
 L  R  R  L  V  P  P  G  L  W  G  S  R  H  N  E  R  R  F  L  R  N  T  K  K  F  I  S  L  G  K  H  A  K  L  S  L  Q  E  L
```

Fig. 11AJ

GACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

CGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCTCAACTACGA
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E

GCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCCGCCGCCTGAGCTGTACTT
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F

TGTCAAG GACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCGTCGGTATGCCGTGGTCCA
V K D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q

GAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGACCAGCCCGCTGAGGGA
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D

TGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGTCCTACGTCCAGTG
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C

CCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCTGCTCCTGCGTTTGGTGGA
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D

TGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAAGACAGTGGTGAACTTCCC
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P

TGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCGACTACTCCAG
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S S

CTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTCACAGCCTGTTTCTGGA
Y A R T S I R A S L T F N R G F K A G R N M R R K L F G V L R L K C H S L F L D

TTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCATCAGCAAGTTTGGAAGAA
L Q V N S L Q T V C T N I Y K I L L L Q A Y R F H A C V L Q L P F H Q Q V W K N

CCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGCGCCGCCGGCCCTCTGCCCTCCGA
P T F F L R V I S D T A S L C Y S I L K A K N A G M S L G A K G A A G P L P S E

GGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCTGACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCAGCTGAGTCGGAAGCTCCC
A V Q W L C H Q A F L L K L T R H R V T Y V P L L G S L R T A Q T Q L S R K L P

GGGGACGACGCTGACTGCCCTGGAGGCCGCAGCCAACCCGGCACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCACAGCCAGGCCGAGAGCAGACACCAGCAGCC
G T T L T A L E A A A N P A L P S D F K T I L D

Fig. 11AK

CTGTCACGCCGGGCTCTACGTCCCAGGGAGGGAGGGGCGGCCCACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCT

GAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCAGGGCCAGCTTTTCCTCAC

CAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGATTCGCCATTGTTCACCCCTCGCCCTGCCCTCCTTTGCCTTCCACCCCCACCATCCAGGTGGAGACCCTGAGAA

GGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAA

AATACTGAATATATGAGTTTTTCAGTTTTGA

Fig. 11AL

Truncated protein that lacks motif A (ver. 2)

```
                    ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTG
                    M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCCGCCGC
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

      GGCCTCCCCGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGGCCGGGGGGAACCAGCGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTG
      G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R
       A S P G S A S G W G * G R P G G T S D M R R A A Q A T Q G A S P A G
        P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V
      |
CCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCG
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGT
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCC
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGC
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCG
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCACCACGCGGGCCCCCC
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAG
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCA
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCG
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTG
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L
```

Fig. 11AM

```
GACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT
 T  W  K  M  S  V  R  D  C  A  W  L  R  R  S  P  G  V  G  C  V  P  A  A  E  H  R  L  R  E  E  I  L  A  K  F  L  H  W  L

GATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
 M  S  V  Y  V  V  E  L  L  R  S  F  F  Y  V  T  E  T  T  F  Q  K  N  R  L  F  F  Y  R  K  S  V  W  S  K  L  Q  S  I  G

AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA
 I  R  Q  H  L  K  R  V  Q  L  R  E  L  S  E  A  E  V  R  Q  H  R  E  A  R  P  A  L  L  T  S  R  L  R  F  I  P  K  P  D

CGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCTCAACTACGA
 G  L  R  P  I  V  N  M  D  Y  V  V  G  A  R  T  F  R  R  E  K  R  A  E  R  L  T  S  R  V  K  A  L  F  S  V  L  N  Y  E

GCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCCGCCGCCTGAGCTGTACTT
 R  A  R  R  P  G  L  L  G  A  S  V  L  G  L  D  D  I  H  R  A  W  R  T  F  V  L  R  V  R  A  Q  D  P  P  P  E  L  Y  F

TGTCAAG                                       GACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCGTCGGTATGCCGTGGTCCA
 V  K                                          D  R  L  T  E  V  I  A  S  I  I  K  P  Q  N  T  Y  C  V  R  R  Y  A  V  V  Q

GAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGACCAGCCCGCTGAGGGA
 K  A  A  H  G  H  V  R  K  A  F  K  S  H  V  S  T  L  T  D  L  Q  P  Y  M  R  Q  F  V  A  H  L  Q  E  T  S  P  L  R  D

TGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGTCCTACGTCCAGTG
 A  V  V  I  E  Q  S  S  S  L  N  E  A  S  S  G  L  F  D  V  F  L  R  F  M  C  H  H  A  V  R  I  R  G  K  S  Y  V  Q  C

CCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCTGCTCCTGCGTTTGGTGGA
 Q  G  I  P  Q  G  S  I  L  S  T  L  L  C  S  L  C  Y  G  D  M  E  N  K  L  F  A  G  I  R  R  D  G  L  L  L  R  L  V  D

TGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAAGACAGTGGTGAACTTCCC
 D  F  L  L  V  T  P  H  L  T  H  A  K  T  F  L  R  T  L  V  R  G  V  P  E  Y  G  C  V  V  N  L  R  K  T  V  V  N  F  P

TGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCGACTACTCCAG
 V  E  D  E  A  L  G  G  T  A  F  V  Q  M  P  A  H  G  L  F  P  W  C  G  L  L  L  D  T  R  T  L  E  V  Q  S  D  Y  S  R

GTGAGCGCACCTGGCCGGAAGTGGAGCCTGTGCCCGGCTGGGGCAGGTGCTGCTGCAGGGCCGTTGCGTCCACCTCTGCTTCCGTGTGGGGCAGGCGACTGCCAATCCCAAAGGGTCAGA
 *

TGCCACAGGGTGCCCCTCGTCCCATCTGGGGCTGAGCACAAATGCATCTTTCTGTGGGAGTGAGGGTGCCTCACAACGGGAGCAGTTTTCTGTGCTATTTTGGTAA.....
```

Fig. 11AN

Lacks motif A and altered C-terminus (ver. 2)

```
ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTG
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCCGCCGC
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

GGCCTCCCCGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGGCCGGGGGGAACCAGCGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTG
G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R
A S P G S A S G W G * G R P G G T S D M R R A A Q A T Q G A S P A G
P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V

CCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCG
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

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G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCC
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGC
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCG
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCACCACGCGGGCCCCCC
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAG
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCA
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCG
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTG
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L
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Fig. 11AO

```
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GATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
 M  S  V  Y  V  V  E  L  L  R  S  F  F  Y  V  T  E  T  T  F  Q  K  N  R  L  F  F  Y  R  K  S  V  W  S  K  L  Q  S  I  G

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 I  R  Q  H  L  K  R  V  Q  L  R  E  L  S  E  A  E  V  R  Q  H  R  E  A  R  P  A  L  L  T  S  R  L  R  F  I  P  K  P  D

CGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCTCAACTACGA
 G  L  R  P  I  V  N  M  D  Y  V  V  G  A  R  T  F  R  R  E  K  R  A  E  R  L  T  S  R  V  K  A  L  F  S  V  L  N  Y  E

GCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCCGCCGCCTGAGCTGTACTT
 R  A  R  R  P  G  L  L  G  A  S  V  L  G  L  D  D  I  H  R  A  W  R  T  F  V  L  R  V  R  A  Q  D  P  P  P  E  L  Y  F

TGTCAAG                                    GACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCGTCGGTATGCCGTGGTCCA
 V  K                                       D  R  L  T  E  V  I  A  S  I  I  K  P  Q  N  T  Y  C  V  R  R  Y  A  V  V  Q

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TGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAAGACAGTGGTGAACTTCCC
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TGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCGACTACTCCAG
 V  E  D  E  A  L  G  G  T  A  F  V  Q  M  P  A  H  G  L  F  P  W  C  G  L  L  L  D  T  R  T  L  E  V  Q  S  D  Y  S  S

CTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTCACAGCCTGTTTCTGGA
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CCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGCGCCGCCGGCCCTCTGCCCTCCGA
 P  T  F  F  L  R  V  I  S  D  T  A  S  L  C  Y  S  I  L  K  A  K  N  A  E
                                                                            |
                                                                          CCGAAGAAAACATTTCTGTCGTGACTCCTGCGGTGCTTGGGTC
                                                                            E  E  N  I  L  V  V  T  P  A  V  L  G  S

GGGACAGCCAGAGATGGAGCCACCCCGCAGACCGTCGGGTGTGGGCAGCTTTCCGGTGTCTCCTGGGAGGGGAGTTGGGCTGGGCCTGTGACTCCTCAGCCTCTGTTTTCCCCCAG
 G  Q  P  E  M  E  P  P  R  R  P  S  G  V  G  S  F  P  V  S  P  G  R  G  V  G  L  G  L  *
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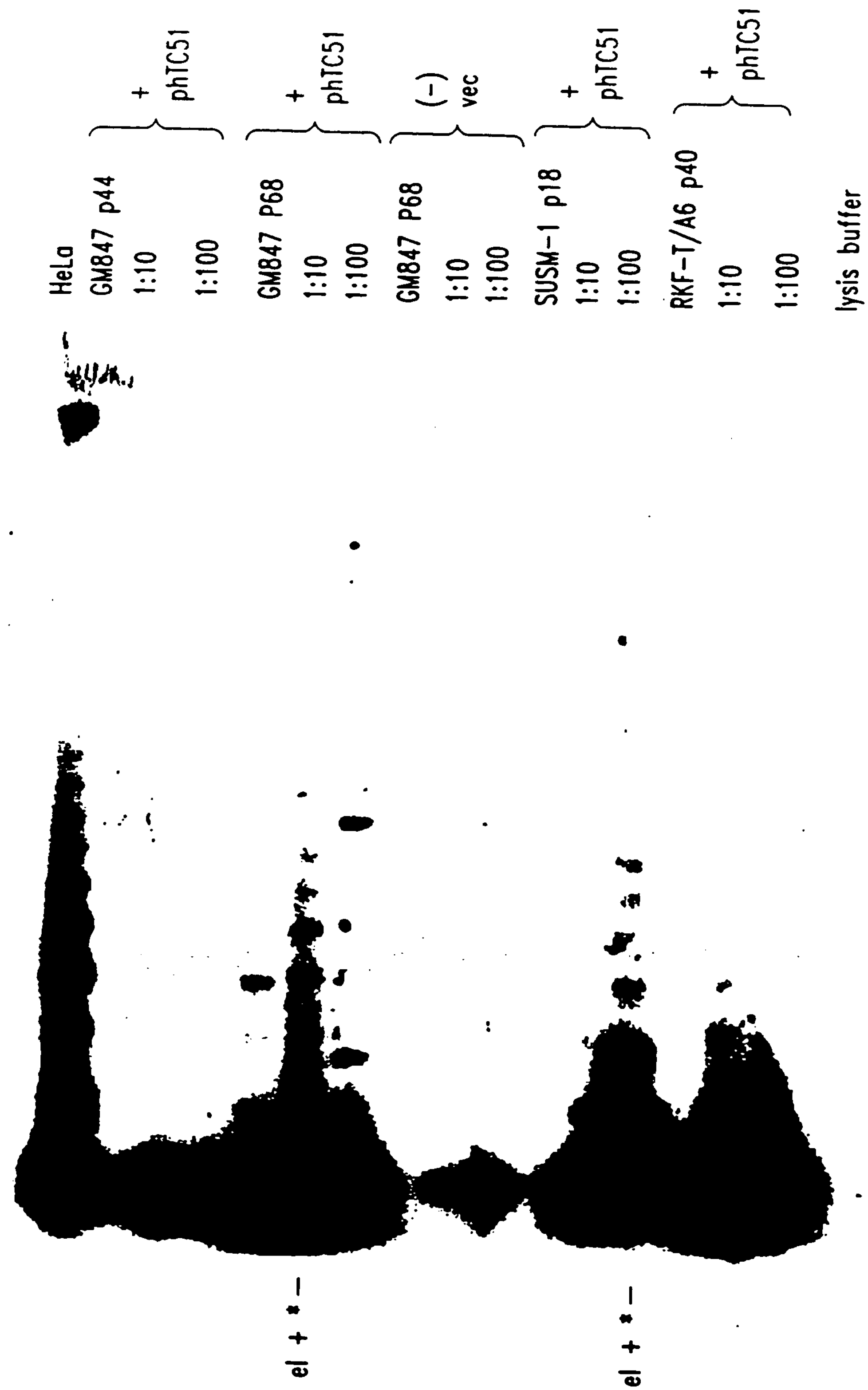
Fig. 11AP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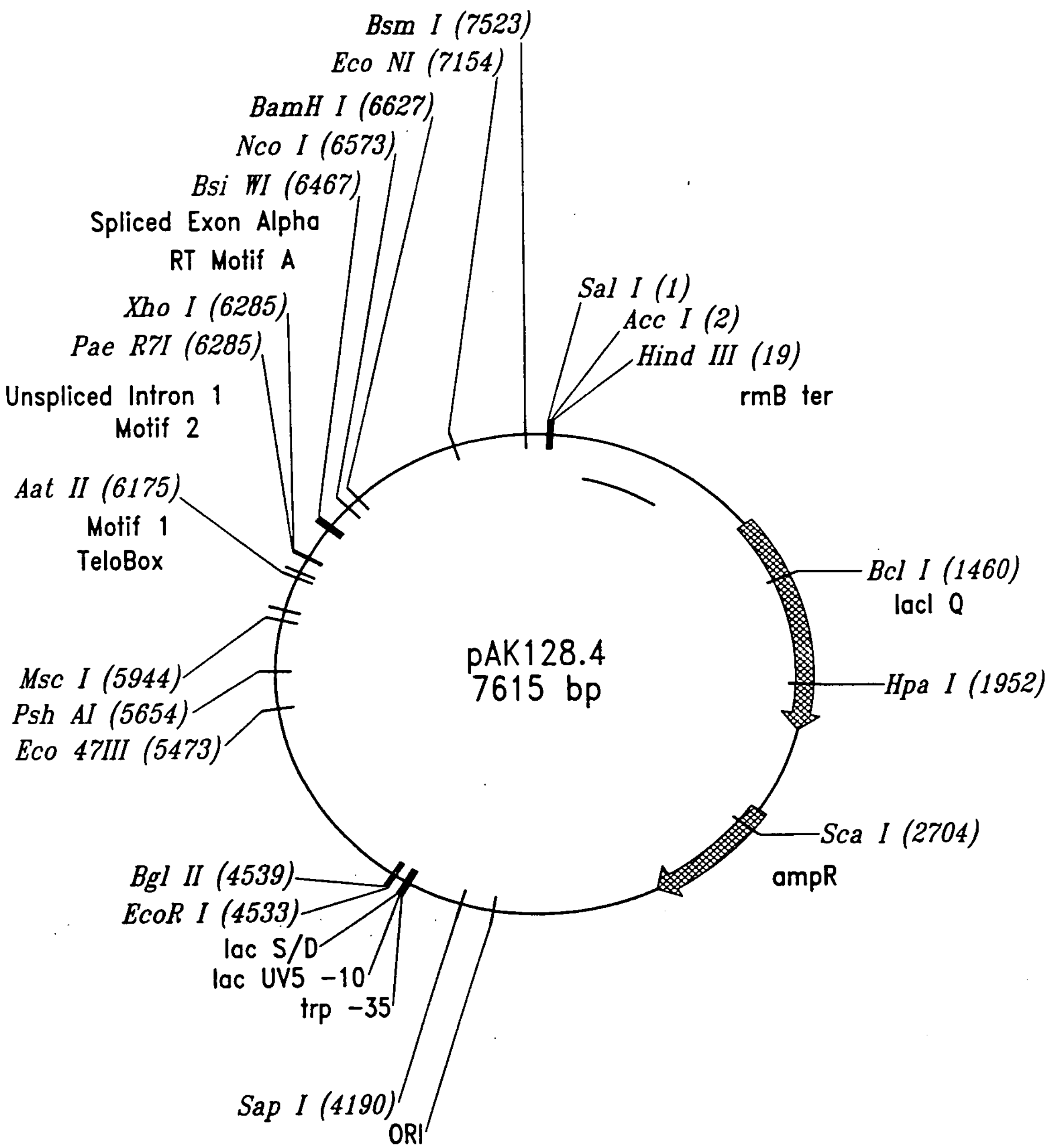
1:100
GM847 P68
1:10
1:100
GM847 P68
1:10
1:100
SUSM-1 p18
1:10
1:100
RKF-T/A6 p40
1:10
1:100
lysis buffer
+ phTC51
+ phTC51
(-) vec
+ phTC51
+ phTC51
el + * —
el + * —

Fig. 12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Eco NI (7154)
BamH I (6627)
Nco I (6573)
Bsi WI (6467)
Spliced Exon Alpha
RT Motif A
Xho I (6285)
Pae R7I (6285)
Unspliced Intron 1
Motif 2
Aat II (6175)
Motif 1
TeloBox
Msc I (5944)
Psh AI (5654)
Eco 47III (5473)
Bgl II (4539)
EcoR I (4533)
lac S/D
lac UV5 -10
trp -35
Sap I (4190)
ORI
Sal I (1)
Acc I (2)
Hind III (19)
rrnB ter
Bcl I (1460)
lacI Q
Hpa I (1952)
Sca I (2704)
ampR
pAK128.4
7615 bp

Fig. 13A

LOCUS pAKI28.4 7615 bp dsDNA Circular
DEFINITION Human telomerase clone with exon beta spliced out

```
   1 tcgacctgca ggcatgcaag cttggcactg gccgtcgttt tacaacgtcg tgactgggaa
  61 aaccctggcg ttacccaact taatcgcctt gcagcacatc ccccttttcgc cagctggcgt
 121 aatagcgaag aggcccgcac cgatcgccct tcccaacagt tgcgcagcct gaatggcgaa
 181 tggcgcctga tgcggtattt tctccttacg catctgtgcg gtatttcaca ccgcataaat
 241 tccctgtttt ggcggatgag agaagatttt cagcctgata cagattaaat cagaacgcag
 301 aagcggtctg ataaaacaga atttgcctgg cggcagtagc gcggtggtcc cacctgaccc
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 481 ttcgttttat ctgttgtttg tcggtgaacg ctctcctgag taggacaaat ccgccgggag
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1501 tggaagctgc ctgcactaat gttccggcgt tatttcttga tgtctctgac cagacaccca
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2641 ttgacgccgg gcaagagcaa ctcggtcgcc gcatacacta ttctcagaat gacttggttg
```

Fig. 13B

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3181 cggggagtca ggcaactatg gatgaacgaa atagacagat cgctgagata ggtgcctcac
3241 tgattaagca ttggtaactg tcagaccaag tttactcata tatactttag attgatttaa
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Fig. 13C

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5701 tgtacggctt cgtgcgggcc tgcctgcgcc ggctggtgcc cccaggcctc tggggctcca
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7021 ggcttcaagg ctgggaggaa catgcgtcgc aaactctttg ggtcttgcg gctgaagtgt
7081 cacagcctgt ttctggattt gcaggtgaac agcctccaga cggtgtgcac caacatctac
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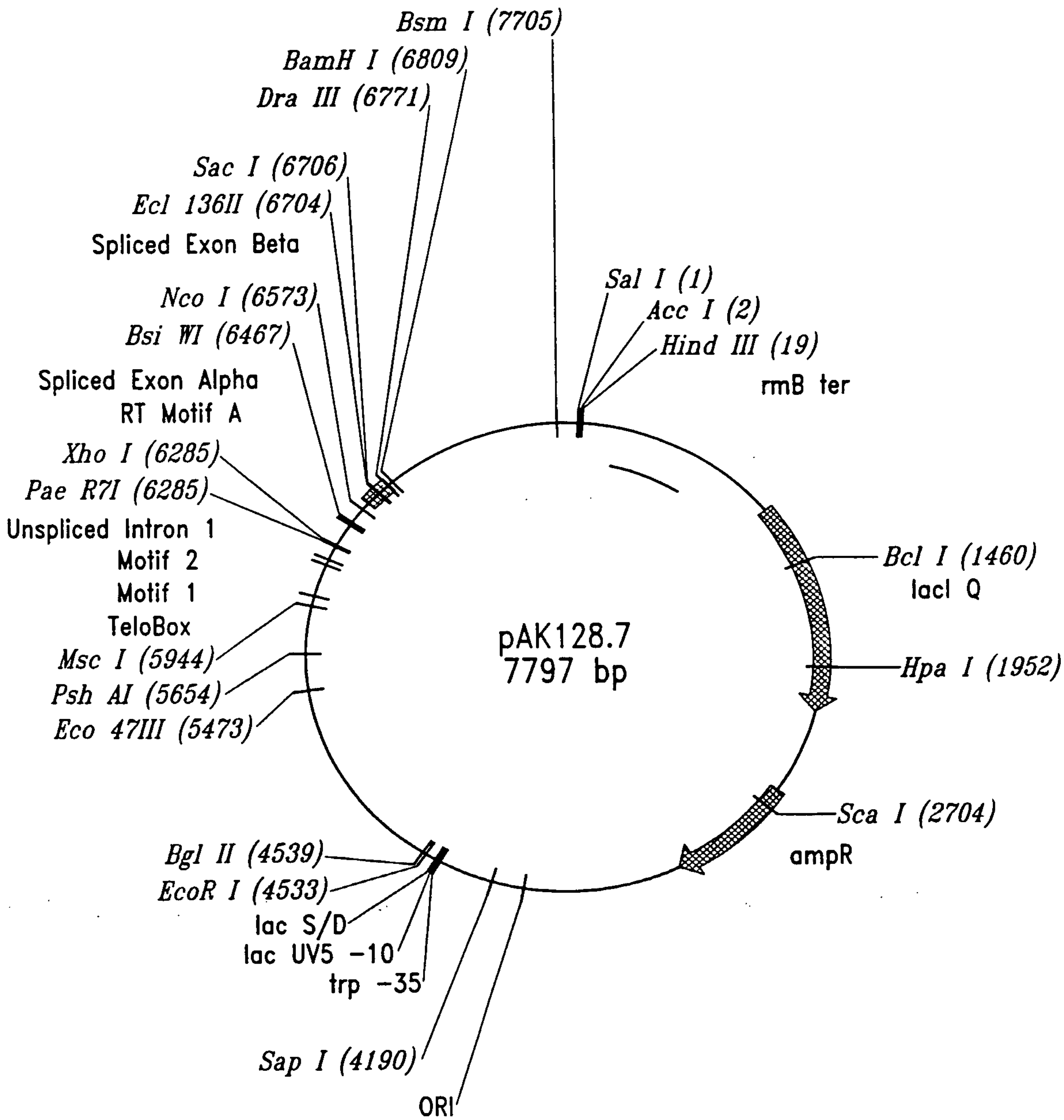
Fig. 13D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BamH I (6809)
Dra III (6771)
Sac I (6706)
Ecl 136II (6704)
Spliced Exon Beta
Nco I (6573)
Bsi WI (6467)
Spliced Exon Alpha
RT Motif A
Xho I (6285)
Pae R7I (6285)
Unspliced Intron 1
Motif 2
Motif 1
TeloBox
Msc I (5944)
Psh AI (5654)
Eco 47III (5473)
Sal I (1)
Acc I (2)
Hind III (19)
rrnB ter
Bcl I (1460)
lacI Q
Hpa I (1952)
pAK128.7
7797 bp
Sca I (2704)
ampR
Bgl II (4539)
EcoR I (4533)
lac S/D
lac UV5 -10
trp -35
Sap I (4190)
ORI

Fig. 14A

LOCUS pAKI28.7 7797 bp dsDNA Circular
DEFINITION Human telomerase clone with alternative C-terminus

```
   1 tcgacctgca ggcatgcaag cttggcactg gccgtcgttt tacaacgtcg tgactgggaa
  61 aaccctggcg ttacccaact taatcgcctt gcagcacatc ccccttttcgc cagctggcgt
 121 aatagcgaag aggcccgcac cgatcgccct tcccaacagt tgcgcagcct gaatggcgaa
 181 tggcgcctga tgcggtattt tctccttacg catctgtgcg gtatttcaca ccgcataaat
 241 tccctgtttt ggcggatgag agaagatttt cagcctgata cagattaaat cagaacgcag
 301 aagcggtctg ataaaacaga atttgcctgg cggcagtagc gcggtggtcc cacctgaccc
 361 catgccgaac tcagaagtga aacgccgtag cgccgatggt agtgtggggt ctccccatgc
 421 gagagtaggg aactgccagg catcaaataa aacgaaaggc tcagtcgaaa gactgggcct
 481 ttcgttttat ctgttgtttg tcggtgaacg ctctcctgag taggacaaat ccgccgggag
 541 cggatttgaa cgttgcgaag caacggcccg gagggtggcg ggcaggacgc ccgccataaa
 601 ctgccaggca tcaaattaag cagaaggcca tcctgacgga tggccttttt gcgtttctac
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 841 gtctgctccc ggcatccgct tacagacaag ctgtgaccgt ctccgggagc tgcatgtgtc
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2641 ttgacgccgg gcaagagcaa ctcggtcgcc gcatacacta ttctcagaat gacttggttg
```

Fig. 14B

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Fig. 14C

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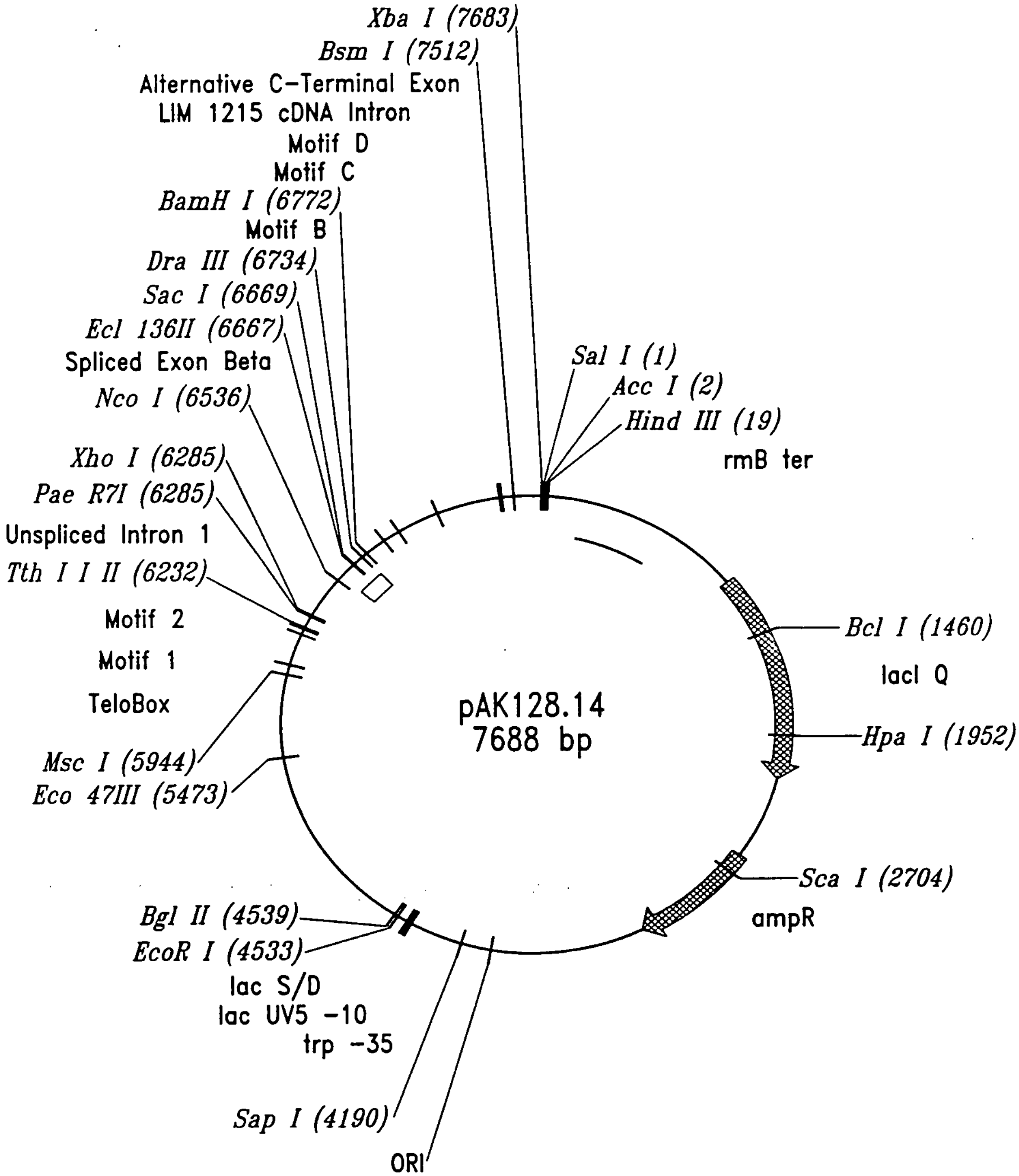
Fig. 14D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Bsm I (7512)
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LIM 1215 cDNA Intron
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BamH I (6772)
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Dra III (6734)
Sac I (6669)
Ecl 136II (6667)
Spliced Exon Beta
Nco I (6536)
Xho I (6285)
Pae R7I (6285)
Unspliced Intron 1
Tth I I II (6232)
Motif 2
Motif 1
TeloBox
Msc I (5944)
Eco 47III (5473)
Bgl II (4539)
EcoR I (4533)
lac S/D
lac UV5 -10
trp -35
Sap I (4190)
ORI
Sal I (1)
Acc I (2)
Hind III (19)
rrnB ter
Bcl I (1460)
lacI Q
Hpa I (1952)
Sca I (2704)
ampR
pAK128.14
7688 bp

Fig. 15A

LOCUS pAKI28.14 7688 bp dsDNA Circular
DEFINITION Human telomerase clone with exon alpha spliced out

```
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  61 aaccctggcg ttacccaact taatcgcctt gcagcacatc cccctttcgc cagctggcgt
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 301 aagcggtctg ataaaacaga atttgcctgg cggcagtagc gcggtggtcc cacctgaccc
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```

Fig. 15B

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3061 cccttccggc tggctggttt attgctgata aatctggagc cggtgagcgt gggtctcgcg
3121 gtatcattgc agcactgggg ccagatggta agccctcccg tatcgtagtt atctacacga
3181 cggggagtca ggcaactatg gatgaacgaa atagacagat cgctgagata ggtgcctcac
3241 tgattaagca ttggtaactg tcagaccaag tttactcata tatactttag attgatttaa
3301 aacttcattt ttaatttaaa aggatctagg tgaagatcct ttttgataat ctcatgacca
3361 aaatccctta acgtgagttt tcgttccact gagcgtcaga ccccgtagaa aagatcaaag
3421 gatcttcttg agatcctttt tttctgcgcg taatctgctg cttgcaaaca aaaaaaccac
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3661 tggctgctgc cagtggcgat aagtcgtgtc ttaccgggtt ggactcaaga cgatagttac
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5461 gcctgcccca gcgctactgg caaatgcggc ccctgtttct ggagctgctt gggaaccacg
5521 cgcagtgccc ctacggggtg ctcctcaaga cgcactgccc gctgcgagct gcggtcaccc

Fig. 15C

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5581 cagcagccgg tgtctgtgcc cgggagaagc cccagggctc tgtggcggcc cccgaggagg
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5701 tgtacggctt cgtgcgggcc tgcctgcgcc ggctggtgcc cccaggcctc tggggctcca
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7681 atctagag
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Fig. 15D